



SEQUENCE LISTING

<110> WOULFE, SUSAN L.  
JAIN, RITA  
BURR, AIMEE

<120> ENGINEERED FAB' FRAGMENT ANTI-TUMOR  
NECROSIS FACTOR ALPHA IN COMBINATION WITH DISEASE MODIFYING  
ANTI-RHEUMATIC DRUGS

<130> 122294-1010

<140> US/10/728,420

<141> 2003-12-05

<150> US 60/431,053

<151> 2002-12-05

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Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
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gta gcc tgg tat cag caa aaa cca ggt aaa gcc cca aaa gcc ctc atc 144  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
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tac agt gcc tct ttc ctc tat agt ggt gta cca tac agg ttc agc gga 192  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
50 55 60

tcc ggt agt ggt act gat ttc acc ctc acg atc agt agc ctc cag cca 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
65 70 75 80

gaa gat ttc gcc act tat tac tgt caa cag tat aac atc tac cca ctc 288  
Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
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gga atg aat tgg gtt aga cag gcc ccg gga aag ggc ctg gaa tgg atg 144  
Gly Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Met  
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Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
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Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
65 70 75 80  
  
ctc caa atg aat agc ctg aga gca gag gac acc gca gtg tac tat tgt 288  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
  
gct aga gga tac aga tct tat gcc atg gac tac tgg ggc cag ggt acc 336  
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Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys  
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<210> 92  
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1 5 10 15  
  
gac agg gtc agc gtc acc tgc aag gcc agt cag aat gtg ggt act aat 96  
Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly Thr Asn  
20 25 30  
  
gta gcc tgg tat caa cag aaa cca gga caa tct cct aaa gca ctg aat 144  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Ala Leu Asn  
35 40 45  
  
tac tcg gca tcc ttc cta tat agt gga gtc cct tat cgc ttc aca ggc 192  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Thr Gly  
50 55 60  
  
agt gga tct ggg aca gat ttc act ctc acc atc agc act gtg cag tct 240  
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Thr Val Gln Ser  
65 70 75 80  
  
gaa gac ttg gca gag tat ttc tgt cag caa tat aac atc tat cct ctc 288  
Glu Asp Leu Ala Glu Tyr Phe Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
85 90 95  
  
acg ttc ggt gct ggg acc aag ctg gag ctg aaa cgt 324  
Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg  
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1 5 10 15  
  
aca gtc aag atc tcc tgc aag gct tct gga tat gtt ttc aca gac tat 96  
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
20 25 30

gga atg aat tgg gtg aag cag gct cca gga aag gct ttc aag tgg atg 144  
Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Ala Phe Lys Trp Met  
35 40 45

ggc tgg ata aac acc tac att gga gag cca ata tat gtt gat gac ttc 192  
Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Val Asp Asp Phe  
50 55 60

aag gga cga ttt gcc ttc tct ttg gaa acc tct gcc agc act gcc ttt 240  
Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Phe  
65 70 75 80

ttg cag atc aac aac ctc aaa aat gag gac acg gct aca tat ttc tgt 288  
Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys  
85 90 95

gca aga ggt tac cgg tcc tat gct atg gac tac tgg ggt caa gga acc 336  
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100 105 110

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Ser Val Thr Val Ser Ser  
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tcgagttcta gataacgagg cgtaaaaaat gaaaaagaca gctatcgcaa ttgcagtggc 60  
cttggctctg acgtacgagt cagg 84

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1 5 10 15

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1 5 10

a atg aag aag act gct ata gca att g 69  
Met Lys Lys Thr Ala Ile Ala Ile  
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Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys \*  
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Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr Leu Gln  
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<223> Synthetic CDP870 Light chain mature protein sequence

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20 25 30  
Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Ala Leu Ile  
35 40 45  
Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Tyr Arg Phe Ser Gly  
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80  
 Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ile Tyr Pro Leu  
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 Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala  
 100 105 110  
 Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly  
 115 120 125  
 Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala  
 130 135 140  
 Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln  
 145 150 155 160  
 Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser  
 165 170 175  
 Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr  
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Val Phe Thr Asp Tyr  
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 35 40 45  
 Gly Trp Ile Asn Thr Tyr Ile Gly Glu Pro Ile Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Phe Ser Leu Asp Thr Ser Lys Ser Thr Ala Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Arg Gly Tyr Arg Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr  
 100 105 110  
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro  
 115 120 125  
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly  
 130 135 140  
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn  
 145 150 155 160

Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln  
165 170 175  
Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser  
180 185 190  
Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser  
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210 215 220  
His Thr Cys Ala Ala  
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<223> Synthetic CDP870 nucleic acid sequence (sense strand)

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accatcaattt gtaaagccag tcagaacgtg ggtactaacg tagcctggta tcagcaaaaa 180  
ccaggttaaag ccccaaaagc cctcatctac agtgctctt tcctctatacg tggtgtacca 240  
tacaggttca gcggatccgg tagtggtaact gatttcaccc tcacgactag tagcctccag 300  
ccagaagatt tcgcccactta ttactgtcaa cagtataaca tctacccact cacattcggt 360  
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